AMENDMENTS TO THE CLAIMS

1. - 3. (Canceled)

4. (Currently Amended) A promoter ~~DNA~~ region comprising a consensus sequence recognized by SigA and a consensus sequence recognized by SigE, which is produced by modifying a nucleotide sequence including a promoter recognized by SigA and bases in the vicinity thereof, to [[be]] further include said consensus sequence recognized by SigE, with ~~the promoter~~ said consensus sequence recognized by SigA being maintained,

wherein the consensus sequence recognized by SigE is a nucleotide sequence comprising a -35 region represented by ATAHTT and a -10 region represented by CATAYAHT, wherein H denotes A, C, or T and Y denotes C or T, which is linked to a site 13 or 14 nucleotides downstream from the -35 region,

wherein the consensus sequence recognized by SigA is a nucleotide sequence comprising a -35 region represented by TTGACA and a -10 region represented by TGNTATAAT, which is linked to a site 14 nucleotides downstream from the -35 region, wherein N represents A, G, C, or T, and

wherein the nucleotide sequence including a promoter recognized by SigA and bases in the vicinity thereof comprises a nucleotide sequence ranging from base Nos. 92 to 552 in SEQ ID NO: 1, a nucleotide sequence ranging from base Nos. 133 to 589 in SEQ ID NO: 2, or a nucleotide sequence having a homology of 80% or more to either of these nucleotide sequences and having the consensus sequence recognized by SigA and/or promoter functions equivalent to those of the consensus sequence.

5. (Previously Presented) The promoter DNA according to claim 4, wherein the nucleotide sequence including a promoter recognized by SigA and bases in the vicinity thereof comprises a nucleotide sequence ranging from base Nos. 92 to 552 in SEQ ID NO: 1, a nucleotide sequence ranging from base Nos. 133 to 589 in SEQ ID NO: 2, or a nucleotide sequence having a homology of 90% or more to either of these nucleotide sequences and having the consensus sequence recognized by SigA and/or promoter functions equivalent to those of the consensus sequence.

6. (Previously Presented) The promoter DNA according to claim 4, wherein the nucleotide sequence having a promoter recognized by SigA and bases in the vicinity of the promoter has a size of 610 bp or less.

7. (Currently Amended) A promoter DNA which is produced by ligating two or more promoter DNAs according to ~~claim 1~~ claim 4.

8. (Currently Amended) An expression vector which has the promoter DNA according to ~~claim 1~~ claim 4.

9. (Previously Presented) A recombinant microorganism which has the expression vector according to claim 8.

10. (Currently Amended) A recombinant microorganism which has the promoter DNA according to ~~claim 1~~ claim 4 on the genome.

11. (Previously Presented) A method for producing a protein or a polypeptide, comprising culturing the recombinant microorganism according to claim 9.

12. (Previously Presented) The method according to claim 11, wherein the protein is cellulase or amylase.

13. (Previously Presented) The method according to claim 12, wherein the cellulase is an alkaline cellulase which has an amino acid sequence of SEQ ID NO: 4, or a protein which has a homology of 70% or more to the amino acid sequence and alkaline cellulase activity.

14. (Previously Presented) The method according to claim 12, wherein the amylase is an alkaline amylase which has an amino acid sequence of SEQ ID NO: 14, or a protein which has a homology of 70% or more to the amino acid sequence and alkaline amylase activity.

15. (Currently Amended) A method for constructing a promoter DNA, comprising modifying a nucleotide sequence having a promoter recognized by SigA and having a nucleotide present in the vicinity of the promoter so as to be recognized by SigA and SigE, wherein said promoter DNA is a promoter DNA according to ~~claim 1~~ claim 4.

16. (Previously Presented) A method for producing a protein or a polypeptide, comprising culturing the recombinant microorganism according to claim 10.

17. (Previously Presented) The method according to claim 16, wherein the protein is cellulase or amylase.

18. (Previously Presented) The method according to claim 17, wherein the cellulase is an alkaline cellulase which has an amino acid sequence of SEQ ID NO: 4, or a protein which has a homology of 70% or more to the amino acid sequence and alkaline cellulase activity.

19. (Previously Presented) The method according to claim 17, wherein the amylase is an alkaline amylase which has an amino acid sequence of SEQ ID NO: 14, or a protein which has a homology of 70% or more to the amino acid sequence and alkaline amylase activity.

20. (Currently Amended) The promoter DNA according to ~~claim 1~~ claim 4, wherein the consensus sequence recognized by SigE is a nucleotide sequence comprising a -35 region represented by ATATTT and a -10 region represented by CATACAAT which is linked to a site 13 or 14 nucleotides downstream from the -35 region.

21. (Currently Amended) The promoter DNA according to ~~claim 1~~ claim 4, wherein the consensus sequence recognized by SigE is a nucleotide sequence represented by ATATTTCAAGTAGTAATAACATACAAT (SEQ ID NO: 19).

22. (Currently Amended) The promoter DNA according to ~~claim 1~~ claim 4, wherein said promoter DNA comprises the nucleotide sequence of SEQ ID NO: 7.

23. (Currently Amended) The promoter DNA according to ~~claim 1~~ claim 4, wherein said promoter DNA comprises the nucleotide sequence of SEQ ID NO: 8.

24. (New) The promoter DNA according to claim 4, wherein the nucleotide sequence including a promoter recognized by SigA and bases in the vicinity thereof comprises a nucleotide sequence ranging from base Nos. 92 to 552 in SEQ ID NO: 1, a nucleotide sequence ranging from base Nos. 133 to 589 in SEQ ID NO: 2, or a nucleotide sequence having a homology of 95% or more to either of these nucleotide sequences and having the consensus sequence recognized by SigA and/or promoter functions equivalent to those of the consensus sequence.

25. (New) The promoter DNA according to claim 4, wherein the nucleotide sequence including a promoter recognized by SigA and bases in the vicinity thereof comprises a nucleotide sequence ranging from base Nos. 92 to 552 in SEQ ID NO: 1, a nucleotide sequence ranging from base Nos. 133 to 589 in SEQ ID NO: 2, or a nucleotide sequence having a homology of 98% or more to either of these nucleotide sequences and having the consensus sequence recognized by SigA and/or promoter functions equivalent to those of the consensus sequence.

26. (New) The method according to claim 13, wherein the cellulase is an alkaline cellulase having an amino acid sequence that has 80% homology or more to the amino acid sequence of SEQ ID NO: 4 and having alkaline cellulase activity.

27. (New) The method according to claim 13, wherein the cellulase is an alkaline cellulase having an amino acid sequence that has 90% homology or more to the amino acid sequence of SEQ ID NO: 4 and having alkaline cellulase activity.

28. (New) The method according to claim 13, wherein the cellulase is an alkaline cellulase having an amino acid sequence that has 95% homology or more to the amino acid sequence of SEQ ID NO: 4 and having alkaline cellulase activity.

29. (New) The method according to claim 14, wherein the amylase is an alkaline amylase having an amino acid sequence that has 80% homology or more to the amino acid sequence of SEQ ID NO: 14 and having alkaline amylase activity.

30. (New) The method according to claim 14, wherein the amylase is an alkaline amylase having an amino acid sequence that has 90% homology or more to the amino acid sequence of SEQ ID NO: 14 and having alkaline amylase activity.

31. (New) The method according to claim 14, wherein the amylase is an alkaline amylase having an amino acid sequence that has 95% homology or more to the amino acid sequence of SEQ ID NO: 14 and having alkaline amylase activity.

32. (New) The method according to claim 18, wherein the cellulase is an alkaline cellulase having an amino acid sequence that has 80% homology or more to the amino acid sequence of SEQ ID NO: 4 and having alkaline cellulase activity.

33. (New) The method according to claim 18, wherein the cellulase is an alkaline cellulase having an amino acid sequence that has 90% homology or more to the amino acid sequence of SEQ ID NO: 4 and having alkaline cellulase activity.

34. (New) The method according to claim 18, wherein the cellulase is an alkaline cellulase having an amino acid sequence that has 95% homology or more to the amino acid sequence of SEQ ID NO: 4 and having alkaline cellulase activity.

35. (New) The method according to claim 19, wherein the amylase is an alkaline amylase having an amino acid sequence that has 80% homology or more to the amino acid sequence of SEQ ID NO: 14 and having alkaline amylase activity.

36. (New) The method according to claim 19, wherein the amylase is an alkaline amylase having an amino acid sequence that has 90% homology or more to the amino acid sequence of SEQ ID NO: 14 and having alkaline amylase activity.

37. (New) The method according to claim 19, wherein the amylase is an alkaline amylase having an amino acid sequence that has 95% homology or more to the amino acid sequence of SEQ ID NO: 14 and having alkaline amylase activity.